SEQUENCE LISTING

5 (1	GENERAL INFORMATION:
10	(i) APPLICANT: Linsley, Peter S Ledbetter, Jeffrey A Damle, Nitin K Brady, William Wallace, Philip M.
МС	(ii) TITLE OF INVENTION: CTLA4 MOLECULES AND IL4-BINDING OLECULES AND USES THEREOF
15	(iii) NUMBER OF SEQUENCES: 14
	(iv) CORRESPONDENCE ADDRESS:
	(A) ADDRESSEE: Merchant & Gould
20	(B) STREET: 11150 Santa Monica Blvd., Suite 400
	(C) CITY: Los Angeles
$\langle V \rangle$	(D) STATE: California
DA	(E) COUNTRY: United States
25	(F) ZIP: 90025-3395
E Lui	(v) COMPUTER READABLE FORM: \
#11.j	(A) MEDIUM TYPE: Floppy\disk
30	(B) COMPUTER: IBM PC compatible
	(C) OPERATING SYSTEM: PC-DOS/MS-DOS
30	(D) SOFTWARE: PatentIn Release #1.0, Version #1.25
	(vi) CURRENT APPLICATION DATA:
	(A) APPLICATION NUMBER:
	(B) FILING DATE:
35	(C) CLASSIFICATION:
	(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Adriano, Sarah
- (B) REGISTRATION NUMBER: 34,470

(C) REFERENCE/DOCKET NUMBER: 9643	
(ix) TELECOMMUNICATION INFORMATION:	
(A) TELEPHONE: (310) 312-9900	
5 (B) TELEFAX: (310) 479-8340	
(B) Indiffice (310) 173 6816	
(2) INFORMATION FOR SEQ ID NO:1:	
(i) SEQUENCE CHARACTERISTICS:	
(1) SEQUENCE CHARACTERISTICS: (A) LENGTH: β9 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: \linear	
(-)	
(ii) MOLECULE TYPE: DNA (genomic)	
(1) AND THE TOTAL OF THE PARTY	
(111) HYPOTHETICAL: NO \	
(iv) ANTI-SENSE: NO	
20	
(vi) ORIGINAL SOURCE:	
(A) ORGANISM: Homo\sapiens	
(A) ORGANISM: Homo sapiens (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:	
25 (xi) SEQUENCE DESCRIPTION: \SEQ ID NO:1:	
(XI) SEQUENCE DESCRIPTION: SEQ ID NO.1.	
CTAGCCACTG AAGCTTCACC ATGGGTGTAC TGCTCACAC)
(2) INFORMATION FOR SEQ ID NO:2: \	
30	
(i) SEQUENCE CHARACTERISTICS: \	
(A) LENGTH: 39 base pairs \	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single \	
35 (D) TOPOLOGY: linear	
79	

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	(ii) MOLECULE TYPE: DNA (genomic)	
	\		
	(iii) HYPOTHETICAL: NO		
_	OFNER, NO		
5	(iv) ANTI-SENSE: NO		
	(vi) ORIGINAL SOURCE:		
	(A) ORGANISM: Homo	sapiens	
	(A) SAGIMIZENS ESSAS	•	
10	(xi) SEQUENCE DESCRIPTION	1: SEQ ID NO:2:	
ŗ	TGGCATGGGC TCCTGATCAG GCTTAGA	AAGG TCCGGGAAA	39
	\		
	(2) INFORMATION FOR EQ ID NO):3:	
<u>1</u> 5	\		
15	(i) SEQUENCE CHARACTERIS	STICS:	
*	(A) LENGTH: \$9 base		
43.74	(B) TYPE: nucleic		
	(C) STRANDEDNESS:		
11 2.0	(D) TOPOLOGY: Line		
2	` `		
ļuk Fili	(ii) MOLECULE TYPE: DNA	(genomic)	
Hard Hard			
a land	(iii) HYPOTHETICAL: NO	\	
25	,		
-01.9	(iv) ANTI-SENSE: NO		
	,		
	(vi) ORIGINAL SOURCE:		
	(A) ORGANISM: Homo	sapi\ens	
30	• •		
	(xi) SEQUENCE DESCRIPTION	on: seq to no:3:	
		\	
	TTTGGGCTCC TGATCAGGAA AATGC	CTTG CTTG&TTGT	39
35		\	

	(2) INFORMATION FOR SEQ ID NO:4:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 84 base pairs	
_	(B) TYPE: nucleic acid	
5	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
	(2) 1920200	
	(ii) MOLECULE TYPE: DNA (genomic)	
10	(iii) HYPOTHETICAL: NO	
(6)	(iv) ANTI-SENSE: NO	
My the)	
' V	(vi) ORIGINAL SOURCE:	
End.	(A) ORGANI\$M: Homo sapiens	
0		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:	
20		60
ļub -	AAGCAAGAGC ATTTTCCTGA TCAGGAGCCC AAATCTTCTG ACAAAACTCA CACATCCCCA	84
i i i	CCGTCCCCAG CACCTGAACT CCTG	04
#1.1 #1.2		
	(2) INFORMATION FOR SEQ ID NO:5:	
25		
ų.į	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 41 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
30	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
	(iii) HYPOTHETICAL: NO	

	(iv) ANTI SENSE: NO	
	(vi) ORIGINAL SOURCE:	
	(A) QRGANISM: Homo sapiens	
5		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:	
		41
	CTTCGACCAG TCTAGAAGCA TCCTCGTGCG ACCGCGAGAG C	•-
10	(2) INFORMATION FOR SEQ ID NO:6:	
6 ,	(i) SEQUENCE CHARACTERISTICS:	
1/2/1	(A) LENGTH: 47 base pairs	
'ν'	(B) TYPE: nucleic acid	
1.5	(C) STRANDEDNESS: single	
11.5	(D) TOPOLOGY: linear	
# 10 # 10 # 10 # 10	(ii) MOLECULE TYPE DNA (genomic)	
1.5 mg tong to game in 1. com in 1.	(iii) HYPOTHETICAL: NO	
	(iv) ANTI-SENSE: NO	
2	COURCE.	
	<pre>(vi) ORIGINAL SOURCE: \ (A) ORGANISM: Homo sapiens</pre>	
25	(A) ORGANISM. Homo Depart	
	(xi) SEQUENCE DESCRIPTION SEQ ID NO:6:	
	CATTGCACAG TCAAGCTTCC ATGCCCATGG GTTCTCTGGC CACCTTG	47
30		
	(2) INFORMATION FOR SEQ ID NO:7:	
	(i) SEQUENCE CHARACTERISTICS:	
35	(A) LENGTH: 39 base pairs	
33	82	
	02	

	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: single
	(D) TOPOLOGY: linear
5	(ii) MOLECULE TYPE: DNA (genomic)
	(iii) HYPOTHETICAL: NO
1.0	(iv) ANTI-SENSE NO
10 4	(vi) ORIGINAL SOURCE:
الم	(A) ORGANISM: Homo sapiens
	(A) Short-
V	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
15	ATCCACAGTG CAGTGATCAT TTGGATCCTG GCATGTGAC
# 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	(2) INFORMATION FOR SEQ ID NO:8:
20	(i) SEQUENCE CHARACTER STICS:
40	(A) LENGTH: 65 base pairs
a Loi	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: single
	(D) TOPOLOGY: linear
	(B) 1010101
49	(ii) MOLECULE TYPE: DNA (genomic)
	(iii) HYPOTHETICAL: NO
30	(iv) ANTI-SENSE: NO
	(vi) ORIGINAL SOURCE:
	(A) ORGANISM: Homo sapiens
	(22)
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:

	CTCAGTCTGG TCCTTGCACT CCTGTTTCCA AGCATGGCGA GCATGGCAAT G	CACGTGGCC	60
	CAGCC		65
	(2) INFORMATION FOR SEQ ID NO:9:		
5	(i) SEQUENCE CHARACTERISTICS:		
	(A) LENGTH: 33 base pairs		
	(B) TYPE: nucleic acid		
	(C) STRANDEDNESS: single		
10	(D) TOPOLOGY: linear		
1854	(ii) MOLECULE TYPE: DNA (genomic)		
10 M	(iii) HYPOTHETICAL: NO		
15	(iv) ANTI-SENSE: NO		
	(vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens		
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:		
# 	(XI) SEQUENCE PERSON		
Hand British Arm	TTTGGGCTCC TGATCAGAAT CTGGGCACGG TTG	33	
25	(2) INFORMATION FOR SEQ ID NO 10:		
	(i) SEQUENCE CHARACTERISTICS:		
	(A) LENGTH: 72 base pairs		
	(B) TYPE: nucleic acid		
30	(C) STRANDEDNESS: single	12	
	(D) TOPOLOGY: linear		
	(ii) MOLECULE TYPE: DNA (genomic)		
35	(iii) HYPOTHETICAL: NO 84		

	(iv) ANTI-SENSE: NO	
	(1V) ANTI-SENSE: NO	
	ODICINAL SOURCE:	
	(vi) ORIGINAL SOURCE: (A) ORÇANISM: Homo sapiens	
	(A) ORGANISM: Nome Express	
5	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:	
	(XI) SEQUENCE DESCRIPTION DEL	
	CTAGCCACTG AAGCTTCACC AATGGGTGTA CTGCTCACAC AGAGGACGCT GCTCAGTCTG	60
		72
10	GTCCTTGCAC TC	
	(2) INFORMATION FOR SEQ ID NO:11:	
,6	(i) SEQUENCE CHARACTERISTICS:	
J. 41.	(1) SEQUENCE CHARTELE (A) LENGTH: \$3 base pairs	
	(B) TYPE: nucleic acid	
T.5	(C) STRANDEDNESS: single	
tij H	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
20	(11) 1101111	
2.0	(iii) HYPOTHETICAL: NO \	
i Luit	(===/	
ilj en	(iv) ANTI-SENSE: NO	
2	(vi) ORIGINAL SOURCE:	
13.	(A) ORGANISM: Homo saptens	
30	(xi) SEQUENCE DESCRIPTION: SEQ D NO:11:	
	GCAATGCACG TGGCCCAGCC TGCTGTGGTA GTG \	
•		
	(2) INFORMATION FOR SEQ ID NO:12:	
35		

	\	•
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 45 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
5	(D) TOPOLOGY: linear	
	l and description	
	(ii) MOLECULE TYPE: DNA (genomic)	
	70	
	(iii) HYPOTHETICAL: NO	
10	NO	
	(iv) ANTI-SENSE:\NO	
5	COUPCE:	
1/2/2/2	(vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens	
"\)	(A) ORGANISM. Homo Dapas	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:	
11 <u>1</u> 11.2 11.0	(XI) SEQUENCE BESS-/	
- P	TGATGTAACA TGTCTAGATC AATTGATGGG AATAAAATAA	45
5 E	TGATGIAACA 101011101101	
	(2) INFORMATION FOR SEQ ID NO:13:	
20	(2) INI OIGHT 2000	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 561 base pairs	
	(B) TYPE: nucleic acid	
25	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (ganomic.)	
30	(iii) HYPOTHETICAL: NO	
	(iv) ANTI-SENSE: NO	
	(vi) ORIGINAL SOURCE:	
35	(A) ORGANISM: Homo sapiens	
	86 \	

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	((ix)	FEAS	ru k e:	:												
	(A) NAME/KEY: CDS																
			(B) гф	CATIO	on:	15	51									
5				,	\												
J		(xi)	SEQ	UENC	E DE	SCRI	PTIO	N: S	EQ I	D NO	:13:						
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	GCA	ልጥር	CAC	GTG	GCC (CAG	CCT	GCT	GTG	GTA	CTG	GCC	AGC	AGC	CGA	GGC	48
	Ala	Met	His	Val	Ala	Gln	Pro	Ala	Val	Val	Leu	Ala	Ser	Ser	Arg	Gly	
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	> m0	CCC	àCC	ափա	GTG	Д СТ	GAG	ТАТ	GCA	TCT	CCA	GGC	AAA	GCC	ACT	GAG	96
5	ATC	310	Cor	Dha	Val	CAR	Glu	Tyr	Ala	Ser	Pro	Gly	Lys	Ala	Thr	Glu	
Np .	TTE	Ala	Ser	20	VUI	7	-	- 4	25					30			
\mathcal{V}				20		\											
15			a=2		GTG	Cmm/	\ccc	CAG	GCT	GAC	AGC	CAG	GTG	ACT	GAA	GTC	144
1.3	GTC	CGG	GTG	ACA	Val	LOU	250	Gln	Ala	Asp	Ser	Gln	Val	Thr	Glu	Val	
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20	TGT	GCG	GCA	ACC	Tyr	ATG	Mat	\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\	, Acn	Glu	Leu	Thr	Phe	Leu	Asp	Asp	
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######################################	TCC	ATC	TGC	ACG	GGC	ACC	TCC	AG	GGA	AAI	. Chn	Val	Asn	Leu	Thr	ATC Ile	
25	Ser	Il€	e Cys	Thr	Gly			Sei	c/GTÀ	ASI	75		11011			Ile 80	
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	CAA	GG	A CTC	G AGO	G GCC	ATC	GAC	: AC	G GGI	A/CTO	TAC	. ATC	. 160	Tue	val	G GAG	1)
30	Glr	n Gl	y Lei	ı Arç	g Ala	Met	: Asp	Th	r Gly	y Le	u Tyi	C TT6	e Cys	У	95	l Glu	
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	ATT 3	71 A (T)	CMA	א עזיתי	G) T	CCA	GAA	CCG	TGC	CCA	GAT	TCT	GAC	TTC	CTC	CTC	384
	Ile :	TAT	Val	Tle	ASIO	Pro	Glu	Pro	Cys	Pro	Asp	Ser	Asp	Phe	Leu	Leu	
	ire.	ıyı	115	110				120	_				125				
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5	TGG :	ATC	CTT	GCA	GCA	GTT	AGT	TCG	GGG	TTG	TTT	TTT	TAT	AGC	TTT	CTC	432
_	Trp	Ile	Leu	Ala	Ala	Val	Ser	Ser	Gly	Leu	Phe	Phe	Tyr	Ser	Phe	Leu	
		130					135					140					
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	CTC	ACA	GCT	GTT	TCT	TTG	AGC	AAA	ATG	CTA	AAG	T.VS	Ara	Ser	Pro	Leu	
10	Leu	Thr	Ala	Val	Ser		Ser	гуѕ	met	ьеи	155	цγо	**** 9	5		160	
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1/2 P	202	202	ccc	ርጥር	ጥልጥ	GTG	AAA :	ATG	CCC	CCA	ACA	GAG	CCA	GAA	TGT	GAA	528
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15	1111		U-1		165			\		170	1				175		
15																	561
	AAG	CAA	TTT	CAG	CCI	LAT '	TTT	ניד/A י	CCC	ATC	LAA I	?					201
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			(1)	SEQU	A) LI	ENGT	H: 1	87 ar	nino	acio	ds						
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25				•	•	OPOL	OGY:	lin	ear								
ŧij.			(ii)	MOL	ECUL:	E TY	PE:	prot	ein	'	\						
			(xi)	SEQ	UENC	E DE	SCRI	PTIO	N: S	EQ. I	J 7/O	:14:	s S	r Se	r Ar	a Glv	
	Ala	a Me	t Hi	s Va	l Al		n Pr	O AT	a Va	ı va	о т пе	u Al	a se	1 50	1	g Gly 5	12
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	1		- 0-	⊶ Dh	. Va	l Cv	rs G1	u Tv	r Al	a Se	r Pr	:o \G1	у Гу	s Al	a Th	r Glu	
	116	9 A.I	a se		20		5 0-	<u>.</u>	2	:5				3	0		
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35	Va:	l Ar	g Va	al Th	nr Va	al Le	eu Ai	cg G]	n Al	la As	sp Se	er Gl	Ln\Vā	al Th	ır Gl	u Val	-
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			35					40					45		•	
<u>.</u>	Cys	Ala 50	Ala	Thr	Tyk	Met	Met 55	Gly	Asn	Glu	Leu	Thr	Phe	Leu	Asp	Asp
5	Ser 65	Ile	Cys	Thr	Gly	Thr 70	Ser	Ser	Gly	Asn	Gln 75	Val	Asn	Leu	Thr	Ile 80
10	Gln	Gly	Leu	Arg	Ala 85	Met	Asp	Thr	Gly	Leu 90	Tyr	Ile	Cys	Lys	Val 95	Glu
Sp. Op	Leu	Met	Tyr	Pro 100	Pro	Pro	Tyr	Tyr	Leu 105	Gly	Ile	Gly	Asn	Gly 110	Thr	Gln
15	Ile	Tyr	Val 115	Ile	Asp	Pro	Glu	Pro 120	Cys	Pro	Asp	Ser	Asp 125	Phe	Leu	Leu
	Trp	Ile 130	Leu	Ala	Ala	Val	Ser 135	Ser	Gly	Leu	Phe	Phe 140	Tyr	Ser	Phe	Leu
H H H	Leu 145	Thr	Ala	Val	Ser	Leu 150	Ser	Lys	Met	Leu	Lys 155	Lys	Arg	Ser	Pro	Leu 160
25	Thr	Thr	Gly	Val	Tyr 165	Val	Lys	Met	Prd	Pro \170	Thr	Glu	Pro	Glu	Cys 175	Glu
	Lys	Gln	Phe	Gln	Pro	Tyr	Phe	Ile	Pro	ţle	Asn					